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            94304, USA
On Apr 2, 1999 this sequence version replaced gi:4337172.
* NOTE: This is a "working draft' sequence. It currently
consists of a contigs. The true order of the pieces.
* is not known and their order in this sequence record is
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1 (Dases I to 169546)
Hyman, R.W., Fung. E.L., Olli, F., Rowley, D., Mao, J., Tamaki, T.,
Kurdi, O. B., Conway, A.B. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1613 tactatatcaacaactttgtgtataaaaagggcaagaaattaagcattatcgtgtgtgagcc
1076 ttccaaacgtaactttgaaggaaaagttgattgagattacatccatatttttgtttttca
                                       73809 ITAAGITAATTAATAAATGGTTATITITATTTAATTAAAATGTGAAATATATTATTAT
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is athlitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurdi,O.B., Conway,A.B. and Davis,R.W. Plasmodium falciparum 3D7 chromosome 12
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Plasmodium falciparum
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                  Length 169546;
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                                         1 23466: contig of 23466 bp in length
57 23666: gap of unknown length
57 169546: contig of 145880 bp in length.
Location/Qualifiers
1. 169546
/organism="Plasmodium falciparum"
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Pred. No. 3.2e-08;
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/clone="PFYAC293"
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Best Local Similarity 46.4%;
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Submitted (24-MAR.2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriégsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) on Jul 6, 2001 this sequence version replaced gi:11071938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP001547 144493 bp DNA PRI 06-JUL-2001
Homo sapiens genomic DNA, chromosome 11q clone:RP11-802F5, complete
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1 (bases 1 to 144493)

1 (bases)

2 (bases)

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139.6; DB 9;
No. 3.5e-08;
Smatches 759;
 Score 139.6; I
Pred. No. 3.5e-
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For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum: IMPOFTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc.
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/product="conserved hypothetical protein, UPF0006 family"
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/gene="MALIP3.01"
/note="MALIP3.01"
aa, similarity: UpF0006 family eg to
YBL055C/YBL0512/YBL0511, YBF5_YEAST (418 aa), fasta
scores: opt: 316, E(): 1.1e-12, (33.2% identity in 271
overlap)
                                                                                                                                    ATATATGTTTTATGTTTTATAAATATATATATATGTTTTATGTATTTATATATA 27087
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                               aagaaaataatgctataaaatatgggtcttctttatcaccttcatgataattatgaaaaa
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Plasmodium falciparum MALIP3, complete sequence.
ALO31746
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Plasmodium falciparum
Eukaryota: Alveolata; Apicomplexa;
I (bases 1 to 67970)
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/organism="Plasmodium
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/gene="MAL1P3.01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
rRNA
                                                                                                                                       gene
                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"mkllnnrfvvlcPililffflnSvvlgnnnrnninfhetenaak
Amrkllsgeinsiklidngdelkiklndekhkdstkmdksysfisnleekysgtdlfr
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Loikkrsnikknhnirkmednessfidigsnijdkmfdgyinskkhendlonyinrak
nnnydkiiitctclaeidkslkicetydpegkflylsagyhptncyefidknkheeke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYYNDIKNYFWYRTRYNEDYNIVVDKTFLQNENITSHDDG†SHNLKHLKNVIKNKLTN
MFKYPFFYHKMYYHKNIINKQILSGLLKNVDDNTNKKICFQEHKSNSTYNYNSSHIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKEEYENIHNSSNSTMSNEFKEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKNINFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKRNSLAIIIGNVGSGKSAFFHSILGDFNMTHGNLYIENFFKKMPILYVPQNSWLFMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIRSMILFGNEYNPLIYRYTILOSELLNDLSTIEHGDMKYINDDHNLSKGQKVRICLA
RALYEHYIHMHKLCTDYEKKLIOPNEILDKDLINNKNISSYNNKKSKLVNYNIPFNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDYTRIKLFDEVELNHVKHSNKMIYKEAYFVKGNTESVSFEIDSINKEYIKKMKKKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKEHMNKNNKDNNNNNNSNKDDHININMNDNHRNYNDINLGPNSTDDSPTVSSLGNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YTLDTYTSNNSDKEEIVKPLYKDTHEEFNKSSSMPFVKSSSNMINNPSNFKYEDNSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TILQKQVRYLEYFVILPIISLVTSGICFSMIIYGNITSAIKVHNNILYSILNAPLYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YNNNLGNIINRFIIDISAFDYGFLKRIYKAFFIFFRCILSSLLIIYMIRDCIFIFPFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IILIYFFVFKRFSRGCKEAQRLYLSCHTPLCNIYSNALSGKNIINIYKKNTYHLDVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVITTQTYKEKNENISDKISAIVEYKNVSLSSIINSSQDDESKKKYGIKFENVYVSYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINISQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KITVEGRDIRTYNRKGEDSIIGILAQSSFVFYNWNIRTFIDPYNNFTDDEIVHALKLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLTNDCIRYLSLVRLYLN
                                                                                                                                    NEKDKEYLENLKNKIIKŸPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVQMFN
LPMFLHMRNCSETFFKIVDIYKFLFFRNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTTYKENVGISNKGNKKKKSCONISFLNFLSFDWIRPLINDLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDIQELPNICRNFDVPYYASKLEENLRDIEVEDSEFYSEKNSSNEHVLHHCNSNDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y isflkdfkvfsglvvvmimffhlffballhfyfhlftinlkvslmyflyk inlcsnn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYIINFIKSTKKMEKDSLNENRSLPNVNIYNIMFSDVPSVTFFVTSCINLFNVFVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLKDRLNKKEEIKFTSIIMPLYVYKILISNVANFPNLVNNVMEGIVNIKRLNNYINDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLDNFLIEDILDNVQYEVNIFEIQDKTLKYRGNISEYMEKNNLNITKESHWGYSNLNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYINNFRISYFFKWLINIWASLYIKIFILLLTTYIIMHPHLYASGIIKLYKEKNYVR]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEI
                                                                                                                                                                                                  CSLKSLENINAVKKIPLNLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKVYNVYYHNILWSILKTFKFRIILIISFYILETLIVTLGGKFIDYYMRILEGQKIP\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSFYVFHIKIGSNSVGIAIWLSIALYSAMILFEFLPSLFKSKYLIYRDKRIDNMHHVI
                                                                                                    I I AKK EY EEF I KY FKNEQVENSKMENGNKK I CDGEKDMNNLNEI LLEKNLDT I PGFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14004.
/gene-"MAL1P3.03"
/note-"MAL1P3.03, putative ABC transporter, len: 1822 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       possible cen1, region of very high [A+T] content"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MALIP3.02"
/gene="MALIP3.02"
5005. 5496
/note="MALIP3.02"
/note="MALIP3.02, hypothetical protein, len: 163 aa,
contains possible signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLQKCLMDDNNFYLYLLDDIFTSLDPSISKKIFSNLFCKEDNISFKDNCSF
                                                                                                                                                                                                                                                                 complement(2599. .2610)

//note="potential splice acceptor sequence"

complement(2742. .2747)

//note="potential splice donor sequence, atg/gttaaa"

complement(2849. .2861)

//note="potential splice acceptor sequence"

complement(2984. .2989)

//note="potential splice donor sequence, aaa/gtaaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"hypothetical protein, MAL1P3.02"
/protein_id-"CAB63557.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative ABC transporter"
/protein_id="CAB63558.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKGSISLETYLMYFQQVGFVLLTSVVIFMLISIF
                                                                                                                                                                                                                                            IIKCDDNTIFKERNEPYNIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GI:6594246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="MAL1P3.03"
14884. .20352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .10389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8020.
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                                                                                                                                                                                                                                                                               misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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/product="hypothetical protein, MaL1P3.05"
/product="hypothetical protein, MaL1P3.05"
/protein_id="CAB63560.1"
/db_xref="C1:6594248"
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/translation="MRIKMNSGIFFIKLLICISFICVFECFNKCMISYRKDLLWYSEN
/translation="MRIKMISSENGE"
RNPLHILIGILYVLAAIYVFENFKNFEC"
                                                                                                                                                                                                                                                                                                                                                                                                           /note-"MALIP3.04, conserved hypothetical membrane protein, len: 203 aa, similarity: P. falciparum chromosome 2, prB0110W, 096126 predicted integral membrane protein (255 aa), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"mkksytfinvtilleltilleltyvynydtesktkennikidin
RFKRIIABASEBOXYPWEEDFCLILNEEELIRPEHNDSPYLPEHYENIDKINELSINS
TKIWKETIKKMRONYEKETDNMNHWRDFWHYKWANIYLYKVHKLINITLKDLTNPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QGGCCIISSVHETSNDTKDNDKENISEDKKEDHQQEEMLKTLDKKERKQKEKEMKKEDE
KIEKKKKQEEKEKKKQEKERKKQEKKERKQKEKEMKKQKKIEKERKKKEKKKKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation="MNVLFLSYNICILFFVVCTLNFSTKCFSNGLLKNONILNKSFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKKK EENSEVMSLYKTGQHKPKNATEHGEENLY EEMVSEINNNAQGGLLLSSPYQYRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDNDKENI SEDKKEDHOOEEMLKTLDKKERKQKEKEMKEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISEETNNEIMVPLPSPLTDVTTPEEHKEGEHKEEEHKEGEHKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EHKEEEHKEEEHKKEEHKSKEHKSKGKKDKGKKDKGKHKKAKKEKVKKHVVKNVIEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKDGVEIINLEDKEACEEOHITVESRPLSQPOCKLIDEPEQLTLMDKSKVEEKNLSIQ
RHKYKIILIDEIPIFNLNNSVHDELNSFLIGRAKSFNYIIRNHFPNNTVLIISHHANT
LSCCDYIYYLRKGEITYRCSYEDVKTQSELSHLLEMDD"
23896. .31533
/gene="rnna"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITGFLLNETELEKNKDDNSKSETLLKEEKDEKDDVPTTSNDNLKNAHNNNEISSSTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNI I NVNDKDNENSVDKKKDKKEKKHKKDKKEKKEKKDKKEKKDKKEKKHKKEKKHKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  //OCCE="WALIPS.06, garp, len: 673 aa, similarity: almost
identical to GARP_PLAFF (678 aa), fasta scores: 97.6%
identity in 678 aa overlap"
                                                                                                                                       /note="region containing small subunit, 5.85 and large subunit rRNA genes and spacer regions"
23896. .31533
/gene="rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="potential splice acceptor sequence" complement(32669. .32674)
/note="potential splice donor sequence, aaa/gtatat" join(36657. .36743,36864. .37343)
/gene="MALLP3.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36744. 36749
Note="potential splice donor sequence, aag/gtatga"
3684 - 36863
/note="potential splice acceptor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDDDEDEDEDEEEEEEEEESEKKIKRNLRKNAKI'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="conserved hypothetical membrane protein, MALIP3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(36657, .36743,36864, .37343)
/gene="MALIP3.05"
/note="MALIP3.05" hypothetical protein, len: 188 //codon_start=1
                                                                                                                                                                                                                                                             complement(join(31966. .32476,32675. .32775))% /gene="MALLP3.04" complement(join(31966. .32476,32675. .32775)) /gene="MALLP3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"potential splice acceptor sequence" complement(join(38049. 39995,40210. 40284))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(38049. .39995,40210. .40284))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDKEETITTWIKWIQEDIEYFLFNLOVEWLRILTLELFYKNKE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical garp protein"
/protein_id="CAB63561.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .40209)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(32477. .32486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAB63559.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref-"GI:6594247"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:6594249"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in 191 aa overlap)"
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NIENIKECKKNCRKINYMDDKEEEFVSKKFFVYEYITSNVWKNEFEKAINTLKNKT
KTCLRSRKKYPKEIRNIMGELEDYIDAINDYKKQFKNLYCWSERYIDYKKWLNEMKEY
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sequence, aag/gtaaca"
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                                                                                                                                            Length 67970;
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                                                                                                                                                                 Indels
                                                                                                                                          Score 135.4; DB 3;
Pred. No. 1.2e-07;
1; Mismatches 722;
 donor
       Join (45401. .46396, 46562.
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Join (45401. .46396, 46562.
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Similarity 46.2%;
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AL010162 04-MAY-2000 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. PEMAL3P5 86827 bp DNA INV 04-N Plasmodium faliciparum MAL3P5, complete sequence. AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010206 AL010210 AL139179 EZ. AL034556.3 GI:7711064
HTG; centromere; CTRP protein; initiation factor Serine/threonine protein phosphatase.
malaria parasite P. falciparum.
Plasmodium falciparum

1 (bases 1 to 86827)

Bowman, S., Lavson, D., Basham, D., Brown, D., Chillingworth, T.,

Bowman, S., Lavson, D., Basham, D., Brown, D., Chillingworth, T.,

Churcher, C. M., Craig, A., Davies, R. M., Deviin, K., Feltwell, T.,

Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S.,

Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J.,

Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A.,

Sulston, J.E., Whitehead, S., Skelton, J., Squares, R., Squares, S.,

Barrell, B.G.

Lawson, D., Bowman, S. and Barrell, B.
Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK The complete nucleotide sequence of chromosome 3 of Plasmodium Bowman, S., Skelton, J., Churcher, C., Lawson, D., Quail, M. and falciparum Nature 400 (6744), 532-538 (1999) Unpublished 3 (bases 1 to 86827) to 86827)

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FEATURES

COMMENT

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/note-"potential splice acceptor sequence for exon 7
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/note="PFC0575w, (MAL3P5.1), Hypothetical protein, len: 689
aa, possible signal sequence, revised: added new exon 2"
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NINNLTRIKOVTHKKKSNEFTKENIKOILLHCVFSKIDFKIINNLSYIIKHFOMSNIT
VHSILNQISEKVKEKKDAENYLALHLFLLKDENITLFSMMHIMDFFKSKOKVIECIRD
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SLYYYNKLDNKHNLINEKKLKYFKQINNEHTQOAPTNHTHHNNNNNKKPLDINIHSC
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On May 14, 2001 this sequence version replaced g1:2982535 g1:2882536 g1:2884454 g1:2982554 g1:2982562 g1:2894489 g1:2982572 g1:2982556 g1:2894489 g1:2982572 g1:2982574 g1:4943931.

For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
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/note="PFC0580c (MAL3P5.2), Hypothetical protein, len:
1097 a, possible signal sequence, predicted using
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/gene="PFC0575w, MAL3P5.1"
/gene="Predictors applice donor sequence for exon 2 of
Proto575w (revised)"
complement(1354. .6644)
/gene="PFC0580c, MAL3P5.2"
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/gene="PFC0575w, MAL3P5.1"
/note="predicted splice acceptor sequence for exon
(revised of PFC0575w)"
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/protein_id="CAB38969.2"
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/protein_id="CAB38968.1"
                                                                                                                                                                                                  'organism-"Plasmodium falciparum"
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/chromosome="3"
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Join(7669. .7717,7800. .7829,7912. .7940,8064, .8106, 8302. .8368,8568. .8641,8713. .8812,8924. .9006,9122. .9258,9369. .9505,9613. .9838) .9258, NDÍKTTVTAMKNKMDOLLTTSYSNKKIDTVNASFQWAQSPEYIFLNIKFSHRWSSPGA LKVKDEEIVSKKNNFSFSALSNDSNSVTKKYIVDLTLLDNIIESETKYNFASVGKVVV TLKKEKKKIWNRLLLSKEKYPUMQVWMDMKEKRIHIITFVTINLFFLLSLSHRYHDSV QNFLKEEKNNSDKLQDDIDEDEEKYFDEEILREAKKKSEEYDKDDEEL" YKNKIKKYITYLNNNISNDLYPYNISYNKIYNONKYKNRKNESHIFYSLKNDIHLLLF LYTORIQNCCDIFSYIYKKYNFNEKNPFLNYLYYBLHYIVYSEKKKKKFFSFISSSP /translation-"MKKKKKHYFSIKFVNVDKNKYVLCSKDYIRIINYMIGLHIFRLL nnniyngdiknnniifkkkynlfessiisyfyikdiyeynyklrlyyiydnlikkfcr IDIVK FKDLYYCMINNINNI FSY IHKVDHNECVY RIFKAYNK ILLY EYNY LNEKENIY **YSYDTMVNSFTFSYFFFSLSYLLFILFYHPDMYASYIFFKTLTYSGLPTYYYSLYNNI** QKIFHIYFANEQIASSFFESHKNYRVTKEDIIDGIEKCWFNITDYLISESIKQDNDFS of exon 2 of note="potential splice acceptor sequence for exon 3 of splice acceptor sequence for exon 5 of splice acceptor sequence for exon 4 of protein, len: 324 aa, splicing prediction very join(7669. 7717,7800. 7829,7912. .7940,8064. .8106, 8302. .8368,8568. 8641,8713. .8812,8924. .9006,9122. 9369. .9505,9613. .9838) /gene="PFCO581w" exon 6 ٥ţ of ğ ō note-"potential splice donor sequence for exon 2 splice donor sequence for exon 3 splice donor sequence for exon 4 splice donor sequence for exon splice acceptor sequence for 'note-"potential splice acceptor sequence for /product-"hypothetical protein, PFC058lw" /protein_id="CAB90285.1" /db_xref="G1:7711066" /note="PFC0581w, hypothetical revised: new gene prediction, 9107. .8112 /gene="PFC0581w" /note="potential s 8293. .8301 /gene="PFC0581w" /note="potential 'note-"potential 8055. .8063 /gene="PFC0581w" /note="potentlal /note="potential PFC0581w" 7901. .7911 /gene="PFC0581w" 8369. .8374 /gene="PFC0581w" 8559 .8567 /gene="PFC0581w" 7830. .7835 /gene="PFC0581w" 7941. .7947 /gene="PFC0581w" 7790. .7799 /gene="PFC0581w" /codon_start=1

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             for exon
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/gene="PFC0581w"
/note="potential splice donor sequence for PFC0581w"
                                                                                                                                                                        /note="potential splice donor sequence for PFC0581w"
                                                   'note-"potential splice acceptor sequence
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Best Local Similarity 46.3%; Pred. No. 1.3e-07;
Matches 585; Conservative 0; Mismatches 670; Indels
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/gene="PFC0581w"
                                                                                                                                                           9259. .9264
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Hattori,M., 18hii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fuliyama,A., Yada,T., Totoki,Y., Matanabe,H. and Sakaki,Y. Direct Submission
Submitted (12-FEB-2000) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1
Kitasato, Sagaminara, Kanagawa 228-8555, Japan
(E-mall:hattoriggsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Chis sequence version replaced gi:7077189.
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Bukaryogian

Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.

Hobses 1 to 173915)

Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Published Only in DataBase (2000) In press

(bases 1 to 173915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP001254 173915 bp DNA PRI 17-MAR-2000
Homo sapiens genomic DNA, chromosome 21q21.1-q21.2, clone;B66B12,
LL56-APP region, complete sequence.
                                                                                                                                                                                                                                                           tatottaatataaacatttgttaatttt-ttotattttagaccatttotttttttt 1445
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1147 atggaaaattaaaatgcacacaaaatgatgtatgagattaaaccaaagtttatcgttatt 1206
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                                                                gaattetttattaaaaaaccaacaaattttaaaacttgtttgcaatagaeccaatatag
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1. .173915
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                                                                                                                     Length 173915;
                                                                                                                                                30;
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Park, H.S., Toyoda, A., Ishli, K., Totoki, Y., Choi, D.K., Soeda, E.,
Ohki, M., Takagi, T., Sakaki, Y., Taudien, S., Blechschmidt, K.,
Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lehmann, R.,
The DNA sequence of human chromosome 21. The chromosome 21 mapping and sequencing consortium
Nature 405 (6784), 311-319 (2000)
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Park, H.S., Toyoda, A., Ishli, K., Totoki, Y., Choi, D.K., Soeda, E.,
Ohki, M., Takagi, T., Sakaki, Y., Taudian, S., Blechschmidt, K.,
Polley, A., Menzel, U., Delabar, J., Kumpf, K., Lebmann, R.,
Patterson, D., Retchwald, K., Rumpf, K., Schillhabel, M., Schudy, A.,
Zimmermann, W., Rosenthal, A., Kudoh, J., Shibuya, K., Kawasaki, K.,
Asakawa, S., Shintani, A., Sasaki, T., Nagamine, K., Mitsuyama, S.,
Antonarakis, S.E., Minoshima, S., Shimizu, N., Nordsiek, G.,
Hornischer, K., Barandt, P., Scharfe, M., Schoen, O., Desario, A.,
Reichelt, J., Kauer, G., Bloecker, H., Ramser, J., Beck, A., Klages, S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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acgtaactttgaaggaaaagttgattgagattacatccatatttttgtttttcatattga 1141
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Homo sapiens genomic DNA, c
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AP001678.1 GI:7768693
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'rpt_family="LTR/Retroviral"
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/rpt_type=DSPERSED
|11744. .11946
/note="MER8"
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'rpt_type=Dispersed
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'rpt_type=TANDEM
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/rpt_type=DisPERSED
complement(10248. 10367)
/note="LiME1"
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complement(9962. .10247)
                        /rpt_type=DisperseD
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complement(7845. 8207)
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/rpt_type=DisperseD
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The chromosome 21 mapping and sequencing consortium consisting of RIKBN Genomic. Sciences Center, Human Genome Research Group, * Sagamihara 228-8555, Japan, * e.mail: hattori@gsc.riken.go.jp
                                                               Direct Submission
Submitted (10-APR-2000) to the DDBJ/EMBL/GenBank databases. The
Stromosome 21 Mapping and Sequencing Consortium: *RIKEN Genomic
Sciences Center, Human Genome Research Group * Institute of
Molecular Biotechnology, Genome Analysis * Keio University School
of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome
Analysis * Max-Planck Institute for Molecular Genetics (addresses
Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * Kelo University School of Medicine, Molecular Biology, * Tokyo 160-8352, Japan.

• e.mall: nshimizu@dmb-med kelo.ac.jp

• URL: http://www.dmb.med.kelo.ac.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@gbf.de
* URL: http://genome.gbf.de/
                                                                                                                                                                                                                                                                                                                                                                                         * Institute of Molecular Biotechnology, Genome Analysis, Beutenbergstrasse 11, D-07745 Jena, Germany, * e.mail: gscj-submit@genome.imb-jena.de * URL: http://genome.imb-jena.de/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Max-Planck Institute for Molecular Genetics,
Innestrasse 73, D-14195 Berlin, Germany,
e.mail: Info-chr21@molgen.mpg.de
URL: http://chr21.rz-berlin.mpg.de/
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Chromosome="21"
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chromosome-"21"
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13925. 13947
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Homo sapiens
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Xiony, H., Zhou, Y., Dong, H., Lin, W., Chen, B., Zhang, C., Zhang, Y.,

Xiony, H., Zhuy, H.F., Wang, H., Gu, W., Zhu, G., Tu, Y., Zhang, X., Jia, J.,

Shen, H., Zhang, D., Wu, C., Lu, G., Zhong, M., Jiang, H., Ren, S., Fu, G.,
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                                                                                                                            tatotaaaaatttgattoocaatatagaacaaattotoaaaatgaacaaacatttgaat 1021
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Homo sapiens chromosome 3 clone RPI1-785A7 map 3p, complete
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                                                                  2 (bases I to 172805)
2 hang, X., Hu, S., Dong, W., Wang, J., Zhang, X., Zhang, H., Liu, B.,
Bao, W., Sun, Y., Wu, Q., Wang, Y., Cheng, C., Wang, Y., Niu, Y.,
Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y.,
Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D.,
Huang, F., Zhang, G., Li, J., Blan, X., Zhang, M., Li, L., Feng, X., Yu, J.
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                                                                                                                                                                                                                                                                  Submitted (25-APR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beljing, 100101, P.R.China
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Submitted (11-FEB-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing,
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On Feb 11, 2001 this sequence version replaced gi:8101281.
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Quality coverage: 8.12x in Q20 bases;sum-of-contigs
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Pred. No. 1.46
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33397 c 32927 g 52715
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/db_xref="taxon:9606"
Chen, Z. and Huang, M.
Chromosome 3p genomic sequence
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6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 29, 2001 this sequence version replaced g1:14718366.
All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [1 chases 1 to 172666]
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens chromosome 18, clone RP11-815K11
------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the finished sequence as soon as it is available and accession number will be preserved.

1 68842: contig of 68842 bp in length
                                                                       Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                         1604 gctagatattactatatcaacaactttgtgtataaaaagggcaagaaat 1652
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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/clone_11b-"RPCI-11 Human
52004 a 31849 c 33483 g 55197
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/organism="Homo sapiens'
/db_xref="taxon:9606"
/chromosome="18"
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Burren, B. Linton, L., Bousbaun, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Bousbaun, C., Lander, E., Allen, N., Campopiano, A., Conepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, S., Ferrellano, R., Dewar, K., Diaz, J.S., Galdge, S., Faro, S., Ferrellano, M., Graham, L., Grand-Pierré, N., Grand-Pierré, N., Grand-Pierré, N.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                    atatottaatataaacatttgttaattttttctattttagaccatttctcttattttat
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Homo saplens, clone RP11-72A1, complete sequence.
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note-"Poly A region that contains some Background noise."
         Marquis,N., Matthews,C., McCarthy,M., McEwah,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Nell,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Sougnez,C., Sentos,R., Schauer,S., Schuback,R., Scamen,S., Schauer,S., Schuback,R., Scamen,S., Strauss,N., Taravis,M., Travis,M., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Tillio,J., Vassillev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
                                                                                                                                                                                                                                                           Submitted (27-DEC-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 24, 2000 this sequence version replaced gi:11597092. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                               ....... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Macdonald, P.,
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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7391. .17700
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23836. .23877
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)37. .2616
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/rpt_family="12"
complement(49283. .49426)
/rpt_family="MIR"
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                                              family="MIR"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 326924)
Materston, R.H.
The sequence of Homo sapiens clone
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                                                                                                      68947 AAATATAAATATAATTTATATATTTATATTTTTATATTTCTATATTTATATAA 69006
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Homo saptens chromosome UNK clone RP11-505B3, *** SEQUENCING IN
PROGRESS ***, 42 unordered pleces.
                                                                                                                                                  ttaataaatattttgattttattttgatatatttgtatttagataacaaaattaagattta 1374
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AC093082.1 GI:15144475
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note="assembly_name:Cont1g21"
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note="assembly_name:Contigll"
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note="assembly_name:Contigl6"
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db_xref="taxon:9606"
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clone="RP11-505B3"
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                                                                                                                                                                                                                                                                        Length 326924;
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                   99613. .105968

106059. .112079

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1012180. .118180

/note="assembly_name:Contig43"

118231. .126420

/note="assembly_name:Contig44"

126511. .134015. .134015

/note="assembly_name:Contig46"

143513. .151892 name:Contig46"

143513. .151892 name:Contig46"

164853. .179948

/note="assembly_name:Contig48"

164853. .179948

/note="assembly_name:Contig48"

164853. .179948

/note="assembly_name:Contig48"

164853. .179948
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Matches 540; Conservative
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                                                                                                                            attttgatatattttgtattttagataacaaaattaagatttaaatattattttatatctta 1393
ttaaaatgcacacaaaatgatgtatgagattaaaccaaagtttatcgttattgaattctt 1214
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Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malaria parasite P. falciparum.
Dassmodium falciparum
Eukaryota: Alveolata: Apicomplexa: Haemosporida: Plasmodium.
(bases 1 to 104992)
                                                               ttattaasasasccaacaaaattttaaaacttgtttgcaatagaccaatatagttaatcca
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                                                                                                                                                                                                                                                                                                                     On Apr 2, 1999 this sequence version replaced g1:4337172.

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ubitary.

Idn.R.W., Qin.F., Fung.E.L., Conway,A.B. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 58642: contig of 58642 bp in length

58842: gap of unknown length

3 91011: contig of 32169 bp in length

2 1211: gap of unknown length

2 104992: contig of 13781 bp in length.

Location/Qualifiers
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AUTHORS
TITLE
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/organism="Plasmodium falciparum

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                                                                                         Gaps
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                         others
                                                                                        Indels
                        405
                                                                Score 132.2; DB 2;
Pred. No. 2.6e-07;
0; Mismatches 818;
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                     9564 9 41411
db_xref="taxon:5833"
           /chromosome="
9326 c 9
                                                                7.68;
                                                                                  Matches 717; Conservative
                                                                          Similarity
                    44286 a
                                                               Query Match
                   BASE COUNT
ORIGIN
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DNA HTG 12-AUG-2000 chromosome 12 clone 3D7, *** SEQUENCING
                                                                                                                                                                                                                                                            Eukaryota; Alveolata; Apicomplexa; Haemospórida; Plasmodium
| Chases 1 to 1695466|
Hyman, R.W. Fung.E.L., Olin,F., Rowley,D., Mao,J., Tamaki,T.,
Kurdi,O.B., Conway,A.B. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                **NOTE: This is a 'working draft' sequence. It currently **NOTE: This is a 'working draft' sequence. It currently ** consists of 2 contigs. The true order of the pieces ** is not known and their order in this sequence record is ** arbitrary. Gaps between the contigs are represented as ** arbitrary. Gaps between the contigs are represented as ** This record N, but the exact sizes of the gaps are unknown. ** This record will be updated with the finished sequence ** as soon as it is available and the accession number will ** be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-FEB-1998) Stanford DNA Sequencing and Center, Stanford University, 855 California Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. Direct Submission
                                                                                                                                                                                                                                                                                                                                      Kurdi,O.B., Conway,A.B. and מעניה, אייי.
Plasmodium falciparum 3D7 chromosome 12
                             ACUU4157 169546 bp DNA
Plasmodium falciparum chromosome
PROGRESS ***, 2 unordered pieces.
                                                                                                                                                                                                          malaria parasite P. falciparum
Plasmodium falciparum
                                                                                                                                                       AC004157.8 GI:9797712
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 169546)
                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
RESULT 13
AC004157/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
                                                                             DEFINITION
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85789 TAATITAATAATTAAATATTTAATAGTAATTAAATATTAAACAAATAATATAAAT
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                                                                                                                                                                                 Length 169546;
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                          in length
                                                                                                                                  others
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contig of 23466 bp in gap of unknown length contig of 145880 bp in
                                                                                                                                                                                  Score 132.2; DB 2;
Pred. No. 2.5e-07;
0; Mismatches 818;
                                                       1. .169546
Organism=Plasmodium falciparum"
/db.xref="taxon:5833"
/chromosome="12"
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                                          Location/Qualifiers
                                                                                                                                  69871 a 15381 c 15705 g
                                                                                                         /clone-"PFYAC293"
 23466:
23666:
169546:
                                                                                                                                                                                 al Similarity 46.0%;
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23467
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188930)
Waterston, R.H.
                                                                                                           85429 AATTAAAATAAAATAACCATTTATTAATTAACTTAATTAATATATATAAAATAAAATT 85370
                                                                                                                                                                                1015 ttgaaattotogatatagaaaacatttacttattttgaattgggacatattocaaagttt 1074
                                                                                                                                                                                                                                                                                            1247 tttgcaatagaccaatatagttaatccatcgtggtctattgtagataaattgtaatattt 1306
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Submitted (27-MAY-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Aug 9, 2001 this sequence version replaced g1:14329170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC091742 188930 bp DNA HTG 09-AUG-200 HOMO sapiens chromosome UNK clone RP11-1220K2, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                         1075 attccaaacgtaa-----ctttgaaggaaaagttgattgattacatccatattt
                                                                                                                                                tgtttttcatattgaatttcatggaaaattaaaatgcacacaaaatgatgtatgagatta
                                                                                                                                                                                                                                            AC091742.4 GI:15144365
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of Homo sapiens clone Unpublished
2 (bases 1 to 188930)
Waterston, R.H.
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AC091742/c
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AUTHORS
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40864 TAATATAACATATATATATATACATATAATATAACATATATATATATATATACATATA 40805
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Center: Washington University Genome Sequencing Center
Center code: WIGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 185000; agarose-fp
Insert size: 190285; sum-of-contigs
Quality coverage: 9.07 in 020 bases; sum-of-contigs
Quality coverage: 8.82 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25971: contig of 25971 bp in length 26071: gap of unknown length 45054: contig of 18983 bp in length 45154: gap of unknown length 109288: contig of 64134 bp in length
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9 188930: contig of 79542 bp in length.
Location/Qualifiers
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                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                     Chemistry: Dye-primer ET; 2% of reads
Chemistry: Dye-terminator Big Dye; 98% of rea
Assembly program: Phrap; version 0.990319
Consenus quality: 187487 bases at least Q40
Consenus quality: 188079 bases at least Q20
Consenus quality: 188370 bases at least Q20
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vector_side.right"
45155. __109288
/note="assembly_name:Contigl1"
109389. __188930
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/note-"assembly_name:Cont1g9"
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/note-"assembly_name:Cont1g10
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                                                                                               Center project name: H_NH1220K02
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/db_xref="taxon:9606"
/chromosome="UNK"
                                                                                                                                                                                                                       Sequencing vector: M13; 17%
Sequencing vector: plasmid; 83%
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YNTEREPROYKKTCPYTIKIRCHENENIKTIKYLCDH
KYDVQYKYSGNNYLKRPKEIHTNSFLDYEKEFGYCFDTSYSNIEBAYVLMSNYLLNYK
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DLPKTFYNYKCIIVGEDNUNDERKKKSTYLYLGKNEDPGYLLSAKIISESAISLIKEN
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 12029)
Gardnar, M.J. Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L.,
Shonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J.,
Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,
Salazberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.,
Salazh, H.O., Fraser, C.M., Hoffman, S.L., et, al.
Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTDFLRNIPKPKKKAYDDENELHDFKESNNSIKKKEEIKKKNQC
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/note="identified by sequence similarity; putative"
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6741. 8021
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Submitted (02-NOV-1998) The Institute for Genomic
Medical Center Drive, Rockville, MD 20814, USA
Location/Qualifiers
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/gene="PFB0875c"
complement(join(471. .1902,2155. .2171))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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/gene-"PFB0885w"
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/protein_id-"AAC71964.1"
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/protein_id="AAC71965.1"
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join(9295. .9298
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2 (bases 1 to 12029)
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Copyright (c) 1993 - 2000 Compugen
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    nucleic search, using sw model

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electron-transfer group, useful as labels in . for genotyping, allowing repeat analyses on

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              The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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Best Local Similarity 1.9%; Pred. No. 3.4e-29;
Matches 15; Conservative 617; Mismatches 177; Indels
                                                                     Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
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                                                      monitoring gene expression.
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Conservative 617; Mismatches 177; Indels
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Pred. No. 3.4e-29;
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gene expression; ss.
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AAF58259/c
ID AAF58259 standard; DNA; 936
XX
AC AAF58259;
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Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
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Pred. No. 3.4e-29;
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                                              ETM; mismatch; genotyping;
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Best Local Similarity 1.9%; Pred
Matches 15; Conservative 617;
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17-MAR-2000; 2000US-0190259
         24-APR-2001 (first entry)
                                             Electron transfer group; gene expression; ss.
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface
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Length 938;
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617; Mismatches 177;
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Local Similarity 1.9%;
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Best Local S:
Matches 15
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BP.

AAF58255 standard; DNA; 938

(first entry)

24-APR-2001

AAF58255;

Oligonucleotide D1876

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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on

(CLIN-) CLINICAL MICRO SENSORS INC

WPI; 2001-159728/16

Umek RM;

26-JUL-1999; 99US-0145695. 17-MAR-2000; 2000US-0190259. 26-JUL-2000; 2000WO-US20476

Example 6; Page 127; 159pp; English

single surface

The present invention relates to a composition comprising two nucleivacids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.

Seguence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

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                                                                                                                                                                                     ttaaatattattttatatcttaatataaacatttgttaattttttctattttagaccatt
                                                                                                                                                                                                                                                                                                                                        Query Match 16.0%; Score 278.2; DB 22; Length Best Local Similarity 0.9%; Pred. No. 4.3e-29; Matches 7; Conservative 613; Mismatches 161; Indels
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17-MAR-2000; 2000US-0190259.
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group; ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 278.2;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, 823 aattttttcattttcgaaattgttctatacaatataaaatataaattttaccacttcgt 882 Gaps ő Length 936; Indels DB 22; Ouery Match 16.0%; Score 278.2; DB 22; Best Local Similarity 0.9%; Pred. No. 4.3e-29; Matches 7; Conservative 613; Mismatches 161; Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other; Example 6; Page 127; 159pp; English.

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useful as labels in

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(CLIN-) CLINICAL MICRO SENSORS INC

WPI; 2001-159728/16.

Jmek RM;

26-JUL-1999; 99US-0145695. 17-MAR-2000; 2000US-0190259.

Nucleic acids containing electron-transfer group, useful as labels 1 hybridization assays, e.g. for genotyping, allowing repeat analyses a single surface

Example 6; Page 128; 159pp; English.

The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,

Sequence 936 BP; 6 A; 138.C; 8 G; 8 T; 776 other;

monitoring gene expression

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genotyping; 5

ETM; mismatch;

Electron-transfer group; gene expression; ss.

26-JUL-2000; 2000WO-US20476

WO200107665-A2

Synthetic.

01-FEB-2001

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17-MAR-2000; 2000US-0190259
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Best Local Similarity 0.9%; Pred. No. 4.3e-29;
Matches 7; Conservative 613; Mismatches 161; Indels
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                                     ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
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                                                                                                                                                                                                                                               Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;
                                                                                                                        Example 6; Page 127; 159pp; English.
                                                                                                                                                The present invention relates to acids each containing an electron
                                                                                                                                                                                                                                                                                                                       Conservative 613;
                                                                                                                                                                                                                          monitoring gene expression.
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Differential gene expression; organelle; mitochondrion; disease state; metabolic state; oybrid coll line; cytoplasmic hybrid; organelle-associated disease; autoimmune disease; hyperproliferative disorder; hyperproliferative disorder; human;
Identifying factor encoded by gene that is differentially expressed comprises comparing expression of genes in cell in first and second
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                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 26A; 176pp; English.
                                                                                                                                       Human UNK22-5' cDNA, SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                   Davis
                                                                                       AAA97340 standard; cDNA; 217 BP.
                                                                                                                                                       Differential gene expression;
                                                                                                                                                                                                                                                                         16-MAR-1999; 99US-0124673.
15-MAR-2000; 2000US-0124673.
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                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                   SW,
                                                                                                                                                                                        Alzheimer's disease; ss.
                                                                                                                                                                                                                                                                                                                  Miller
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                                                                                                                                                                                                          Homo sapiens.
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The invention relates to a method of identifying factors, including organellar factors encoded by genes that are differentially expressed when cells in different states (e.g., metabolic, respiratory, diseased, or apoptotic states) are compared. The invention also encompasses a method of diagnosing a disease by contacting a sample from an individual with the differentially expressed gene product or an antibody which binds to it; and a cell line a cell line a selected from cybrid (cytoplasmic hybrid) cell line 1685, ATCC 207149 or ATCC 207150. The invention also discloses examples of organellar factors which are differentially expressed in organelle-associated disease, including a variety of human genes which are differentially expressed in Alzheimer's disease. The method of the invention is useful for identifying factors which are differentially expressed in organelle-associated diseases as disorders (e.g., Alzhelmer's disease, Parkinson's disease), autoimmune diseases, diabetes mellitus, arthritis, NARP (neuropathy, ataxia, retinitis pigmentosa), Kearns-Sayre disease, Pearson's Syndrome, PEO (progressive external ophthalmoplegia), Wolfram syndrome, Leigh's Syndrome, schizophrenia, stroke, mitochondrial diabetes and deafness (MIDD) and hyperproliferative disorders, such as cancer, tumours and psoriasis. Sequences AAA97298-A97302 and AAA97314-A97350 are cDNAs representing genes found to be differentially expressed in Alzhelmer's disease. include mitochondria-associated diseases such as neurodegenerative compared with the healthy state. The organelle-associated diseases

Sequence 217

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tegatatagaaaacatttacttattttgaattgggacatattecaaagtttattecaaac 1083
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                                  /*tag= a /note= "this region is specifically claimed claim 7b"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G protein coupled receptor flh84g5 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis; single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ng for the presence of polymorphisms associated with inflammatory disease, using a hybridization assay -
                                                                                                                                                                     Gaps
                                                                              Gaps
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                                                                                                                         Human inflammatory bowel disease related gene fragment IGR3319a.
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Pred. No. 8.7e-07;
); Mismatches 297; Indels
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52 T; 0 other;
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                                             DB 21;
1.8e-09;
                                             Ouery Match 7.5%; Score 130; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 130; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 384; 463pp; English
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50.8%;
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Distefano P, Glucksmann MA, (MILL-) MILLENNIUM PHARM INC 98WO-US25832 98US-0042780. 97US-0985090. WPI; 1999-394858/33. P-PSDB; AAY06323. 04-DEC-1998; 17-MAR-1998; 04-DEC-1997;

Goodearl ADJ, Xie M;

New nucleic acid encoding an isolated G-protein coupled receptor useful for treating nervous system related disorders

Claim 7b; Fig 2; 140pp; English.

This nucleotide sequence, the coding region of which is claimed, codes for a novel rat G protein coupled receptor, termed fin8495 (see AAY06323). The fin8495 conk was isolated from a rat frontal cortex CDNA library, and has been used to isolate human fin8495 polyncleotides from including polyncleotides human, rat and mouse transmembrane regions of fin8495 and antisense nucleic acid molecules), expression vectors, host cells, transgenic animals, fin8495 polypeptides and antibodies, and a method of modulating phosphatidylinositol metabolism. The fin8495 polypeptides can a fin8495 ligand, such as acetylicholine or carnitine, (ii) interact with a G protein or another protein which naturally binds to fin8495, (iii) modulate the activity of an ion channel (e.g. a calcium activity acted channel or a potassium or calcium or calcium channel), (1v) modulate cytosolic ion, e.g. calcium concentration, (v) modulate the release of a neurotransmitter, e.g. acception or carnitine from a neuron, (vi) modulate a filhadga acceptioner in a responsive cell, (vii) signal ligand binding via phosphatidylinositol turnover, and (viii) signal ligand binding cattvity. The products can be used to treat: disorders mediated by abnormal filhadga polypeptide activity such as nervous system related disorders, e.g. amnesia, apraxia, agnosia, annestic dysnomia, amnestic spatial disorientation, Kluver-Bucy syndrome, Alizhelmer's related memory loss and learning disability; disorders affecting consciousness such as visual hallucinations, perceptual disputivences or delearium associated with Lewy body domentia, and acceptual epressive illness (primary and secondary); affective disorders uch as REM sleep abnormalities in patients suffering from e.g. epression, paradoxical sleep abnormalities, sleep-wakefulness, and ars e.g. Parkinson's disease related movement disorders; disorders e.g. insulin hypersecretion related obesity or a disorders, e.g. diabetic polydipsia; smooth muscle related isorders, e.g. irritable bowel syndrome, diverticular disease, rinary incontinence, oesophageal achalasia or chronic obstructive disorder such as xerostomia or diabetes mellitus disease; cardiac muscle disorders, e.g. pathologic rdia or tachycardia, arrhythmia, flutter or fibrillation; temperature or respiratory depression abnormalities during disorders affecting pain generation mechanisms e.g. pain ed to irritable bowel syndrome or chest pain; movement products can also be used for detection, diagnosis and drug chitzo-effective disorders, schizophrenia with mood swings screening

Sequence 3244 BP; 609 A; 1052 C; 903 G; 680 T; 0 other;

ö Gaps ö Ouery Match
6.3%; Score 109; DB 20; Length 3244;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: April 2, 2002, 05:37:48 ; Search time 1546.5 Second (without alignments) 12055.561 Million cell	Title: US-09-811-093-42 Perfect score: 1735 Sequence: 1 agcggataacaatttcacactaattggaaagcttgtgagt	Scoring table: IDENTITY_NUC Gapext 1.0	Searched: 11351937 seqs, 5372889281 residues	Total number of hits satisfying chosen parameters: 22703874	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database: EST:* 1: em_estfun:* 2: em_esthum:* 3: em_estin:*	4: em_eston:* 5: em_estpl:* 6: em_estps:* 7: em_estro:*				18: em_gss_pro:* 19: em_gss_rod:* 20: em_gss_vrt:* 21: em_gss_vrt:*	Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.		Result Query No. Score Match Length DB ID	C 1 131.4 7.6 1101 13 CNSO0EVL AL069706 C 2 124.2 7.2 1101 13 CNSO0EVL AL061936 AL061936 4 118.2 6.9 1201 13 CNSO0EVL AL061936 C 5 117.2 6.8 6.25 13 CNSO0EVL AL069706 C 5 115.8 6.7 1101 13 CNSO0EVL AL069706 C 7 115.2 6.8 6.7 1101 13 CNSO0EVL AL061936 AL061936 C 8 115.8 6.7 1101 13 CNSO0EVL AL061936 AL061936 AL061936 C 8 114 6.6 951 13 AZ676519 AL065607 AZ676519

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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACRO5N11 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                                                                                      1033 aaaacatttacttattttgaattgggacatattccaaagtttattccaaacgtaactttg 1092
                                                                                                                                                                          1099 WWIAIWTHTHTWITTHWWIAIWTIAWAIAIAAAWIAAITWWIWIAIAIWIAWWYAIW 1040
                                                                                                                                                                                              1093 aaggaaaagttgattgagattacatccatatttttgtttttcatattgaatttcatggaa 1152
                                                                                                                                                                                                                                       1153 aattaaaatgcacacaaaatgatgtatgagattaaaccaaagtttatcgttattgaattc 1212
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                            559 ТИНТТТАААТТАТИТТТТТТТТТАМАНИНАААМАТИАМИМИМААААЛИМИМТИТ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ctttgtgtataaaaagggcaagaaattaagcattatcgtgtgagccacttttt 1679
                                                                                                               DB 13; Length 1101;
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                                                                                                                                   Indels
                                                                       232
                      melanogaster"
                                                                                                              Ouery Match 7.6%; Score 131.4; DB 13; Best Local Similarity 35.4%; Pred. No. 1.7e-06; Matches 231; Conservative 139; Mismatches 277;
                                                                       ų
                                                                       299
         1. .1101
/organism="Drosophila me/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29B23"
 Location/Qualifiers
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                                                          /note-"end : T7"
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Drosophila n
Eukaryota; h
Pterygota; N
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : Direct Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EYNY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr) - Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Obetermination of this BAC-end sequence was carried dut as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-99 and was constructed by partial Ecok dispession of Drosophila DNA provided by the BDGP from the lisogenic strain y2; cn bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the Ibrary and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://www.iffile.com.edu/drosophila_bac.thm.
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scomorpha; Ephydroidea; Drosophilidae; Drosophila (bases 1 to 1101)
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/db_xref="taxon:7227"
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/clone-"BACR05N11"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Biland at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                  CNSO167M 1201 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15M24 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                             taataactaaatgatgtgacacacactaatattatttttatccaaagaaaataatgctat
                                                                                                                                           tataaacatttgttaattttttctattttagaccatttctctttattttatataacattt
                                                                                  TNNGNNNNGANNTTTTTTTTTTTTTTTTTTTTTAAACTTTCATGAAAACTTT
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/plasmid-"pBeloBAC11"
/db_xref-"taxon:7227"
/clone_lib-"DrosBAC"
/clone="BACN15M24"
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39.4%; Pred. No. 3.9e-05;
:1ve 102; Mismatches 428;
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Matches 349
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DNA GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BAC29BAZ3 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                             617 TKTTTTKTTTGTTTTTTANGCTTTAKKKTKGTKTTTKBTTKKTKTTTTGKKKKKKKKKTKK 676
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                     atacca---aatctaaacgatcgkataccaaatctaaatgatcatgtaccaaatatatt
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aaataataaatcggttagatttggctatccaaatttaaatgaccaaatctaaacgatcgt
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr.

Wab: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2: cn bw sp, the same strain used for the BDGP's pland BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://www.fac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="texon:7227"
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/clone="BACR29B33"
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Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a lar
scale clone-end sequencing project of the Terracdon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracdon.
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215D15 of library G from Tetraodon nigroviridis, genomic survey
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Pred. No. 9e-05;
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/db_xref="taxon:99883"
/clohe="215D15"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDCP Drosophila melanogaster BAC library was prepared by Kazutcyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: nbw sp, the same strain used for the BDGP's pl and BST library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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40.6%; Pred. No. 9.7e-05;
Live 60; Mismatches 525; Indels 9;
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR05N11"
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CASULELD 1225 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence SP6 end of BAC
BACNISCI8 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106171
AL106171.1 GI:5620504
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                                                                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRX cedex - FRANCE (E-mail .: seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 TKNNKNNAMNMAKNNKNKNKNNTNNCKKKTKKNNNNCACNCCCCCNCNNCCAKKCKKN 552
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon.7227"
/clone_lib="DrosBAC"
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llarity 29.9%; Pred. No. 0.00011;
Conservative 159; Mismatches 351;
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/note="end : SP6"
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Direct Submission

Direct Submission

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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr

- Web: www.genoscope.cns.fr

- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please. See http://www.fruitfiy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegaw and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the laogenic strain v2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be filters for hybridization from the BACPAC Resource Center can be
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Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone_llb="RPCI-98"
/clone="BACR14H09"
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
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Seg primer: AATTAACCCTCACTAAAGGG
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Fax: 864 656 4293
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// Ab_xref="taxon:5759"
// Ab_xref="taxon:57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: enta@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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   341 aaccaaatctgatttctttctatcgtctttcttctttttctctttttccgctgcga 400
                                                                595 TTIMIYITIWCYCTTITITITITITITITITITITITITITITICACAACAACAAAAAA 536
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                                                                                                                                Entamoeba histolytica.

Entamoeba histolytica.

Eukaryota; Entamoebidae; Entamoeba.

I (bases) to 951)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba I HM1:IMSS sheared DNA library

Contact: Breadan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research
9112 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 11
High quality sequence stop: 279.
Location/Qualifiers
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Hordeum vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frisch, D., Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1151)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yr., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and Wood,T.
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HVSMEc0002A15f Hordeum vulgare seedling shoot EST 11brary.
HVCDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEc0002A15f, mRNA sequence.
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                                                                                                     Length 951;
University Press, 1999)."
45 g 471 t
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Pred. No. 0.00017;
  Barell, Oxford
74 c 4
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BG309087.1 GI:13109934
                                                                                                     Query Match 6.6%;
Best Local Similarity 52.8%;
Matches 246; Conservative
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Unpublished (2000)
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SC 29634, USA

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1 (bases 1 to 485)
Maiti,A.K., Jorrissen,M. and Bouvagnet,P.
Isolation, in slico characterization and chromosomal localization
a group of cDNAs from ciliated epithelial cells
Genome Biol. (2001) In press
Contact: Maiti AK
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .485

// Organism="Homo sapiens"

// Organism="Homo sapiens"

// Organism="ton: 9606"

// Colore_lib="ciliated epithelial cDNA cell library"

// Lissue_type="kasal biopsy"

// cell_type="cultured ciliated epithelial cells after in

vitro ciliopenesis"
                              asatttaattatatatattcatttcatctaatcgtacaagctagatattactatatcaaca 1625
                                                      BG673765 485 bp mRNA EST 01-MAY-2001
905 ciliated epithelial cDNA cell library Homo sapiens cDNA 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory de Genetic Moleculaire Humaine, Faculty of University Cl. Bernard, 8 Avenue Rockfeller, F69373 Lyon cedex, France Tel: (33) 478 77 44 25 Eax: (33) 478 77 5 68 Email: amit_mait_demdecine.unige.ch Seq primer: M13 Forward and reverse.
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Pred. No. 0.00066;
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/note="Vector: PCR2.1; cloned |
isolated total RNA".
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llarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
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                                                                                       1626 actttgtgtataaaaa 1641
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Best Local Similarity
Matches 110; Conserv
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                                                                                                                                                           /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 1 c 100 g 439 t
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                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                            Length 1151;
                                        /organism-"Hordeum vulgare"
/cultivar-"Morex"
/db_xref-"texon:4513"
/clone-"HYBMEC0002A15f"
/clone_1lb-"Hordeum vulgare seedling shoot 1HVCDNNO003 (Etlolated and unstressed)"
/fissue_type-"Seedling shoot"
/lab_host-"TJC121"
                                                                                                                                                                                                                                                                          Ouery Match 6.5%; Score 113; DB 11; Length 1
Best Local Similarity 47.0%; Pred. No. 0.0002;
Matches 402; Conservative 0; Mismatches 441; Indels
   1086.
High quality sequence stop: 1
Location/Qualifiers
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 638)
Petersen,S., Pietas,A., Cheng,Y., Schluens,K., Pacyna-Gengelbach,M., Deutschmannin,N. and Petersen,I.
A genome-wide survey of lung cancer associated genes
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila malanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Site_1:
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                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="H2170-115"
/clone=11b="H2170-115"
/cell_line="H2170"
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/cell_line="H2170"
/lab_host="ropi0f" (ampicillin resistant)"
/note="Organ: lung; Vector: pCR2.1 (Invitrogen); Site_Note="Organ: lung; Vector: pCR2.1 (Invitrogen); Site_sippression subtractive hybridization (SSH)"
suppression subtractive hybridization (SSH)"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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Schumannstrasse 20/21, 10117 Berlin, Germany
Trel: 00433028022611
Fax: 00493028023371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%; Score 110; DB 11;
11arity 100.0%; Pred. No. 0.00057;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                       Email: iver.petersen@charite.de
Insert Length: 638 Std Error:
Seq primer: M13 Forward
POLYA=No.
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                                                                                                                                                                               Institute of Pathology
                                                                                                                                                         Contact: Petersen
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Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoxI digestion of Drosophila DNA provided by the BDGF from the isogenic strain y2: on bw sp, the same strain used for the BDGF PP and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
Aaron Mammoser in Pieter de Jong's laboratory in the Department
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
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Best Local Similarity 39.1%; Pred. No. 0.00044;
Matches 275; Conservative 108; Mismatches 302; Indels
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/clone_lib="RPCI-98"
/clone="BACR29P01"
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Pred. No. 0.00044;
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66 c 104 g
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1479 actaatattattttatccaaagaaaataatgctataaaaatatgggtcttcttatcacc
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Terraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.ons.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcmi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Letraodonridae; Tetraodonridae; Saurin, W., Bernot, A. and Welssenbach, J. Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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cost.Crollius, W. Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="G"
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169 c 165 g 262 t 113 others
                                        CNSO20K7 1092 bp DNA GSS 12-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 222L11 of library G from Tetraodon nigroviridis, genomic survey
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/clone="222111"
                                                                                                                                                   GSS; genome survey sequence. Tetraodon nigroviridis.
                                                                                                                                                                                          Tetraodon nigroviridis
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Best Local Similarity 43.2
Matches 200; Conservative
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AQ934864 430 bp DNA GSS 22-DEC-1999
156_A_09-21 SmBAC1 Schistosoma mansoni genomic clone 156A09 5', DNA
sequence.
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/lab_host="Blomphalaria glabrata": hind III; Partially /note="Vector: pBelobac 11; Site_1: Hind III; Partially /note="Vector: pBelobac 11; Site_1: Hind III digested and size-selected S. manson cercarial DNA was ligated into Hind III digested pBelobac 11 vector and used to transform E. coll DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold."
                                                                                                                                                                                                                                                                                                                                                                            Wu, W., Pierce, R.J., Le Paslier, D., Johnston, D., LoVerde, P.T. and Williams, D.L.
WHO/UNDP/World Bank Schistosoma Genome Initiative: Development of BAC/ARC contig for chromosome 3 of Schistosoma manson!
Unpublished (1999)
Other_GSSs: 156_A.09-rew
Contact: Pierce RJ
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Platyhelminthes; Turbellarian Platyhelminths;
                                                                                                                                                                                                                                                                      Rhabditophora; Eulecithophora; Revertospermata; Mediofusata; Neodermata; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019-Lille, France
17E1: (33) (0)3 20877783
Fax: (33) (0)3 20877888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 430;
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ilarity 100.0%; Pred. No. 0.0012;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Raymond.Pierce@pasteur-lille.fr
Plate: 156 row: A column: 09
Seq primer: M13 -21 primer
Class: BAC ends
High quality sequence stop: 430.
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/strain="Puerto-Rican"
/db_xref="taxon:6183"
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                                                                                                                                                                            Schistosoma mansoni
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, Wed Apr 3 10:09:06 2002

Search completed: April 2, 2002, 07:01:09 . Job time: 5001 sec

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Gencore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 2, 2002, 05:41:13; Search time 91.56 Seconds

(without alignments)
4291.605 Million cell updates/sec

Title:
Perfect score: 1735
Sequence: 1735
Sequence: 1 agoggataacaattCacac......taattggaaagcttgtgagt 1735
Scoring table: IDENTIY_NUC
Gapop 10.0, Gapext.1.0
Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ē	4, Appli	1137, Ap	288, App	14, Appl	13, Appl			2, Appli	2, Appl1	2, Appl1	6, Appli	1, Appli	8, Appli	8, Appli	8, Appli	595, App	14, Appl	534, App	5231168	1137, Ap	683, App	1036, Ap	10, Appl	10, Appl		288, App	1, Appli
Description	Sequence				Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Patent No.	Sequence			Sequence	Sequence	Sequence	Sequence	Sequence
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% Query Match	6.3	5.3	5.2	5.1	5.0	5.0	4.8	4.7	4.4	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.0	4.0	4.0	4.0	3.9
Score	109	92.8	86.8	89.3	87	86.3	84	80.8	76.2	75	74	73.6	73.4	73.4	73.4	73.2	72.6	71.8	71.4	71.2	70.8	70.4	69	69	69	68.8	68.4
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Gaps

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Query Match 6.3%; Score 109; DB 3; Length 3244; Best Local Similarity 100.0%; Pred. No. 4.4e-10; Matches 109; Conservative 0; Mismatches 0; Indels (

; TOPOLGSY: linear ; MOLECULE TYPE: CDNA ; FEATURE: ; NAME/KEY: CDS ; LOCATION: 778..2112 US-09-165-543-4

Appl Appl Appl Appli App				
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Sequence Seq		for		
		Glucksman d Oses Therefor	.25	
2 US-08-883-795A-36 4 US-08-998-416-186 4 US-08-990-571-10 4 US-08-990-571-10 4 US-08-990-571-10 1 US-07-638-431-1 2 US-08-446-855A-1 4 US-08-446-855A-1 4 US-08-446-855A-1 1 US-08-299-415-1 1 US-08-299-953-1 1 US-08-299-953-1 1 US-08-299-953-1 1 US-08-299-953-1 1 US-08-299-953-1 1 US-08-299-953-1 1 US-08-299-953-2 1 US-08-299-953-2 1 US-08-299-953-2 1 US-08-299-953-2	rs	ស្តួ	Version #1.	
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US-08 US-08	æ,	US/09165543 US/09165543 U. Goodearl Muscarinic 39	1ble 5/ms 3/ms 19/1	HATION: HAILON: (1. 33,505 MBER: MNI- ORMATION: 77-7400 4214 NO: 4: IICS: Pairs 116
		S/09.	disk patible Dos/M elease A: US/09/	IATION Hanlon Hanlon HER: WO: NO: ICS: pairs
665 615 701 3701 3701 3701 8920 8920 8920 8920 8920 8821 2861 2861 2861 3881 3881		on US D.J. MUS: Muses VE & VE & e Str	COMPUTER KEADALLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS SOFTWARE: PATCHIN DATA: APPLICATION NUMBER: US/09/1 FILING DATE: CLASSIFICATION: PRIOR APPLICATION: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE: FILING DATE:	ATTORNEY AGENT INFORMATION: NAME: Elizabeth A. Hanley REGISTRATION NUMBER: 33,50; REFERENCE/DOCKET NUMBER: M TELECOMOUNICATION INFORMATION TELEPHONE: (617)227-740 TELEFRAX: 3244 base pairs TYPE: nucleic acid STRANDEDIESS: single TOPOLOGY: linear MOLECULE TYPE: CDN NAME/KEFY. CDS
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		equence 4, Application Usatent No. 6093545 GENERAL INFORMATION: APPLICANT: Andrew D.J TITLE OF INVENTION: M. WUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & STREET: 28 State St: CITY: Boston STREET: Assachusett: COUNTRY: USA	MEDUTER KEADALE FOR MEDIUM TYPE: FLOPPO COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COSTWARE: PATENTION NUMBER: PLING DATE: CLASSIFICATION DATAPLLING NUMBER: PLING DATE: PLING DAT	NAME: Elizabeth A. REGISTRATION NUMBER: ELIZABETH A. REGISTRATION NUMBER: ELECOMONICATION INPORTATION FOR SEQ. IN TELEFRAX: (617)227 TELEFRAX: (617)227 TELEFRAX: (617)224 TELEFRAX: (617)224 TELEFRAX: (617)224 TELEFRAX: (617)224 TELEFRISTI CUNCE CHARACTERISTI LENGTH: 3244 base por STRANDEDNESS: Singl STRANDEDNESS: Singl TYPE: CDN AND CLEVEN CON CONTROL CON AND CLEVEN CON CONTROL CONTROL CON CONTROL CON CONTROL CO
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                                                                                     136 AATTATTATATTATTACTTAATTCATCATTATTAATATT---TATATAATTATAAAAAT 192
TTAAACTATTATTATCATTATTTAATAAATTAATTATTTGATTATTAATACTTATTATAT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCES OF ASHBYA GOSSYPII
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54 Cornwall1s Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
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Wendland, Jurgen
Knechtle, Philip
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION
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Patent No. 623926
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US-08-998-416-288
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                                                  130 AGCGGATAACAAITITCACACAGGAAACAGCTAIGACCAIGATTACGCCAAGCTIGGTACC 189
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                      1 agoggataacaatttcacacaggaaacagctatgaccatgattacgccaagcttggtacc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rebischung, Corinne
/ENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 636;
                                                                                                                                                190 GAGCTCGGATCCACTAGTAACGCCCCCAGTGTGCTGGAATTCGGCTTG 238
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Pred. No. 1.7e-07;
0; Mismatches 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "....see: No. 6239264artis Corporation
FEF: 3054 Cornwallis Road
': Research Triangle Park
E: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LICATION NUMBER: US/08/998,416
ING DATE: 24-DEC-1997
SSIFICATION: 435
                                                                                                                                                                                                                                                               Sequence 1137, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORMATION FOR SEQ ID NO: 1137
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Melgs, J. Timothy REGISTRATION NUMBER: 38,241
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Knechtle, Philip
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: 636 base pairs
nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: US-08-998-416-1137
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                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 TATTAGATATTATTATTTTC-----TTTAATAAATTATTAAATAGATTATCAATAA 303
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5.2%; Score 89.8; DB 4; Length 837;

Best Local Similarity 50.4%; Pred. No. 5.3e-07;

Matches 305; Conservative 0; Mismatches 287: Indela 1
                                                                            PF/5-30306/A/CGC1976
                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8687
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                PAG1241RP
                                                                                                                                                                                                                                                                                                         linear
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Sequence 14, Application US/08232463 Patent No. 5670367

US-08-232-463-14

GENERAL INFORMATION:

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Score 89.2; DB 1; Length 7218;
                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/232,463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 5.1%; Score 89.2; E
Best Local Similarity 5.3%; Pred. No. 7.1e-
Matches 13; Conservative 180; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30472/114 IMMU FELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 91 114 300.6
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-08-487-826B-13/c
; Sequence 13, Application US/08487826B
                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         29,768
                                          SSEE: Foley & Lardner 1: 1800 Diagonal Road, Alexandria
                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703)683-4109
                                                                                                         COUNTRY: USE
ZIP: 22313-029
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                          NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                               ADDRESSEE:
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ATTORNEY/AGENT INFORMATION
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APPLICANT:
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         APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
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; Pred. No. 1.7e-06;
0; Mismatches 485; Indels 1
                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                 ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                       10-SEP-1993
                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIHI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-850
INFORMATION FOR SEG ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match<sup>.</sup>
Best Local Similarity 46.9%
Matches 438; Conservative
                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                          MEDIUM TYPE:
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US-08-487-826B-13
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                                                                                                                                                                                                 COUNTRY:
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APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attttaataactaaatgatgtgacacacactaatattatttttatccaaagaaaataatg 1510
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1153 aattaaaatgcacacaaaatgatgtatgagattaaac-caaagtttatcgttattgaatt 1211
                                                                                                                                                                                                               ATATTAGAGATAACAAAAGAGACAAATATGTTCTTCGTTTCTCTGTATCTATTATCTA 6624
                                                                                                       1212 cttttattaaaaaaccaacaaaattttaaaacttgtttgcaatagaccaatatagttaat
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620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1689 gagatagaaggtttaaaatcatgtototaattg 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6263 TGTTCTATATTTATATAAATGAAATATTTG 6231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/08487826B Patent No. 5993827
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Sim, Kim L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chitnis, Cheta
Miller, Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES; CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Newport Beach
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us-09-811-093-42.rni

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1596 tegtacaagetagatattactatateaceacetttgtgtataaaaagggeeagaaattaa 1655
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                                                                                                   1416 tctattttagaccatttctctttattttatataacattttaataactaaatgatgtgaca 1475
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                                           5743 ATATITATITGEGRATATGTCTGTGTTAAGATAGATATGCATTACAGTTAAGGGTTATAG
                                                                                                                                                                                            1476 cacactaatattattttatccaaagaaaataatgctataaaatatgggtcttctttatc
                                                                                                                                                                                                                                   5803 TITITITITITITITITIGIACATATATAAAAAATAGATAACTAACAATATGCATATT
                                                                                                                                                                                                                                                                                                                       5923 TACTAATAGGTAATTAGTTTTATATATCATCCTTTTAT-----TATTATAATTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: No. 6239264artis Corporation
: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
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TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 186, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
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VENTION: GENOMIC DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Philippsen, Peter APPLICANT: Pohlmann, Rainer APPLICANT: Steiner, Sabine APPLICANT: World, Christine APPLICANT: Knechtle, Philipp
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FELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 919-541-8689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                           Length 19124
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Pred. No. 2.2e-06;
1; Mismatches 614; Indels
                                             NIH121.001CP1
                        29,655
                                                        TELECOMOUNICATION INFORMATION:
TELEPHONE: (619) 235-6550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             5.0%;
                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                          LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Israelsen, Ne
ATION NUMBER:
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US-08-487-826B-13
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                                                                                                                                                                                4.8%; Score 84; DB 4; Lei
llarity 49.8%; Pred. No. 4.5e-06;
Conservative 0; Mismatches 290;
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Patent No. 6280942
: LENGTH; 615 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: ORIGINAL SOURCE:
CREANISM: PAG1074RP
US-08-998-416-186
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 301; Conserva
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1065 TTGTGAAATAACATAACTAGGTCTCATATTTTTAAATAATAATGTATCTTTAGGATTATA 1006
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Pred. No. 1.5e-
1; Mismatches
                                                                     cerevisiae
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 44.4%;
Matches 457; Conservative
                                            TYPE: DNA
ORGANISM: Saccharomyces
                                                                                                               ) NAME/KEY: CDS
) LOCATION: (1)..(1428)
US-09-316-083-2
NO 2
FH: 1431
                        LENGTH:
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                             228 TIGITIAIGATAGITATAATACATTATAATACATATCTAATAATAATAAAATITTATT 169
                                                                                    168 ATTATCCCATTAAAAAAAAAGTCATATTATTCATTAAAAATTTATACATATTTCATA 109
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STREET: One Liberty Place 46th Floor
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Pred. No. 8.9e-
0; Mismatches
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APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    FITLE OF INVENTION: Improved Plas
                                                                                                                                                                                                                Sequence 2, Application US/07867106
Patent No. 5389526
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REGISTRATION NUMBER: 35,134
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Local Similarity 44.0%;
les 469; Conservative
                                                                                                                                                                                                                                                           Slade, Martin B
Chang, Andy C M
Williams, Keith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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EDNESS: single
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COMPUTER READABLE FORM:
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LOCATION:
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COCATION:
US-07-867-106-2
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2470 CAAACGCACATCATTTTTTACAACCTTTGAATTCTTCCAAAAGTATTACAAAAACTT
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1141 aatttcatggaaaattaaaatgcacacaaaatgatgtatgagattaaaccaaagtttatc 1200
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NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,
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STATE:
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                                          GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION DATA:
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2IF: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
PC. Compatible
PC. PC-DOS/MS-D
        Sequence 2, Application US/07867106
Patent No. 5389526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RI
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ilarity 44.9%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS:
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2378..5038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION:
US-07-867-106-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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Best Local Simi
Matches 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH
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1201 gttattgaattottttattaaaaaaccaacaaattttaaaaacttgtttgcaatagacca 1260
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aatattttgatttattttgatatatttgtatttagataacaaaattaagatttaaatat 1380
                                                                                                                                                                                                                                                                                                                                                                  attttatatettaatataaaacatttgttaattttttctattttagaccatttcttttt 1440
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                                                                                                                                                                                                                                        1742 ITITITAGATAGATATAAAATAAATTGCCTATCGATATATATATTTAATTTAAGATTG
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; Sequence 6, Application US/08628417
; Patent No. 5627054
; Patent No. 5627054
; GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
ITILE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
ITILE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 7
CORRESPONDENCES: 7
CORRESPONDENCE ADDRESSE: U.S. ARMY CHEMICAL AND BIOLOGICAL
ADDRESSEE: DEFENSE COMMAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE:
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COUNTRY: US
ZIP: 32606
TOPOLOGY:
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                                                                                                                                                                                                                                Length 240;
                                                                                                                                                                                                                                                                      95; Indels
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APPLICANT: Bradshaw, Marite
APPLICANT: Rood, Julian
TITLE OF INVENTION: Expression System for Clostridium
TITLE OF INVENTION: Species
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 TITITITITITITITITITITAGIAAAATIAITICIAAAGITITAT 15
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                    Score 74; DB 1; 1
Pred. No. 0.00018;
0; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Seay, NICholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95238
                                                                                                                             MOLECULE TYPE: oligodeoxynucleotide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: Quarles & Brady
F: 1 South Pinckney Street
Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09056075
Patent No. 5955368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FELECOMMUNICATION INFORMATION TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                    Query Match 4.3%;
Best Local Similarity 58.0%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6243 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       608-251-9166
                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles &
                                                                                                            linear
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                                                                                                                                                               ; ANTI-SENSE: YES
US-08-628-417-6
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1473 ITTTTATATTCTTTTTTCTTCAAGATTATATATATAAAAAATTTTTTTCAAACTTTAAA 1414
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                                                                                                                                                                                                                                                                                                                                                                                                  1262 tatagttaatccatcgtggtctattgtagataaattgtaatattttgttatatttaatea 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                1413 TAAAAAATTITITATATTITITATTITITTATTITITATTITITATTITITATTITITTTATTITTTATTIT 1354
NAME/KEY: misc_feature

) COCATION: 3770..4013

) OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from

) OTHER INFORMATION: plasmid RP4"

US-09-056-075-1
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US-07-991-867B-8
Sequence 8, Application US/07991867B
Patent No. 54767N-10:
Patent Nover, Richard W.
APPLICANT: Moyer, Richard L.
APPLICANT: Griddl, Michael E.
TITLE OF INVENTION: No. 5476781e1 Entomopoxvirus Expression System NUMBER OF SEQUENCES.
NUMBER OF SEQUENCES.
ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                  Length 6243;
                                                                                                                                                                                               Score 73.6; DB 2; Length E
Pred. No. 0.00023;
0; Mismatches 104; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-PEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1237 ATTTTTTTTTTTTT 1220
                                                                                                                                                                                                     Query Match
Best Local Similarity 58.1%;
Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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1484 tattatttttatccaaagaaaataatgctataaaatatgggtcttctttatcaccttcat 1543
                                    1070 ITTAAATITITATAACAAAATTAAAAATATAACATATITAGATATATCTTATACAAAA 1129
                                                                        DNA (genomic)
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COMPUTER READABLE FORM:
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APPLICANT: MOYEL,
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Best Local Similarity
Matches 355; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                Florida
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: F.
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NAME/KEY:
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FEATURE:
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US-08-107-755A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttaaaccaaagtttatcgttattgaattcttttattaaaaaaccaacaaattttaaaac 1243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 ATAATATCATAAT ----TATCTACGATATTGATTTCATTAATTAAATTATTGTTTTAA 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     884 atattttcgaaaagaccccttaaataaattgaattcgcatataattaaaattttttccca 943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716 TAATITITICGCATCAATICTGTTTTTGCCAGAAAACATAGGACCAATTATTAATTCTA 775
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1004 tgaacaaacatttgaaattctcgatatagaaaacatttacttattttgaattgggacata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 73.4; DB 1;
; Pred. No. 0.00024;
0; Mismatches 401;
                                                                                                                                                                                                               ORGANISM: Amsacta moorei entemopoxvirus
                                                                                                                                                                                                                                                                                                                              complement (234..782)
                                                                                                                                                                                                                                                                        complement (18..218)
       TELECOMMUNICATION INFORMATION
TELEPHONE: 904-375-8100
TELEPAX: 904-372-8800
INFORMATION FOR SEQ ID NO: 8:-
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 46.3%;
Matches 355; Conservative
                                                                                                     LENGTH: 1511 base pairs
                                                                                                                     TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                               CDS
852..1511
                                                                                                                                                           unknown
                                                                                                                                                             POPOLOGY:
                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-07-991-867B-8
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APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 40.
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R c.11.
STREETE OF SECURITIES OF STREETE OF 
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1130 TAGCAATATAAAGTAATATATACTACCACATTCTATAGAATTTTTAA 1176
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PatentIn Release #1.0, Version #1.25
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0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: David R. Saliwanchik
:: 2421 N.W. 41st Street, Suite A-1
Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amsacta moorei entemopoxvirus
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGBNT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 73.4
Pred. No.
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CURRENT APPLICATION NUMBER: US/08/107,755A
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-ANG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (234..782)
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
TELEFAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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                                                                                                                               481 ATTITATCACAAAATIGTICTAAATCATTITCTTCAAAAAATTGACACTCATCTATGCCA 540
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APPLICANT: Maly, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSE: Gerard H. Bencen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1244 ttgtttgcaatagaccaatatagttaatccatcgtggtctattgtagataaattgtaata
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824 attititcatititcgaaatigitciatacaatataaaatataaatatitiaccacticgit
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                                                                                           atattttcgaaaagaccccttaaataaattgaattcgcatataattaaaattttttccca
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2421 N.W. 41st Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08544332
Patent No. 5935777
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2421
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US-08-544-332-8
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NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Amsacta moorei entemopoxvirus
                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
PILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING PAPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
                                                                                                                                                                                                                                                                                      FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
PPLING DATE: 30-5AN-1992
FILING DATE: 30-5AN-1992
PRIOR APPLICATION UNMER: US 07/657,584
APPLICATION UNMER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bencen, Gerard H.
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UF114.C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
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Best Local Similarity 46.3
Matches 355; Conservative
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852..1511
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                                                               APPLICATION NUMBER:
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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LOCATION:
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; LOCATION:
US-08-544-332-8
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1124 ttttgtttttcatattgaatttcatggaaaattaaaatgcacacaaaatgatgtatgaga 1183
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                                                                                                                                                          1244 ttgtttgcaatagaccaatatagttaatccatcgtggtctattgtagataaattgtaata 1303
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                                     716 TAATTTTTCGCATCAATTCTGTTGTTTTGCCAGAAAACATAGGACCAATTATTAATTCTA 775
                                                                                                                                                                                                835 AAAATAAAATTATCAAAATGGATTTACTAAATTCTGATATAATTTTAATAATATTTTAA 894
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Search completed: April 2, 2002, 07:46:30 Job time: 7517 sec